

## SEQUENCE LISTING

<110> Kaneka Corp.  
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 MATSUMOTO, Keiji  
 TAKAGI, Masamichi  
 OHTA, Akinori

<120> NOVEL TRANSFORMANT AND PROCESS FOR PRODUCING POLYESTER USING THE SAME

<130> Q96497

<150> PCT/JP2005/003589  
 <151> 2005-03-03

<150> JP 2004-061291  
 <151> 2004-03-04

<150> JP 2004-062812  
 <151> 2004-03-05

<160> 39

<170> PatentIn version 3.3

<210> 1  
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 <223> chemically-synthesized restriction enzyme cleavage site

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 <223> chemically-synthesized polynucleotide encoding mutant Aeromonas caviae phaC having mutation at codon 149

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<210> 3

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<212> DNA

<213> Artificial Sequence

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<223> chemically synthesized polynucleotide encoding *Ralstonia eutropha* phbB for expression in *Candida maltosa*

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catggtttca ctatggcttt ggcccaagaa gttgccacta aagggtgttac tgtcaatacc 540  
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aaaattgtcg ccaccattcc agtcaaaaga ttggggtttgc cagaagaaat tgcttctatt 660  
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cagatctcga ctctagagga tccccgtttt tttatttccg caatacaaaa ttatttttta 600  
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 35 40 45

Gln Gly Ser Gln Gln Pro Trp Gln Leu Ile Gln Ala Gln Met Asn Trp  
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Trp Gln Asp Gln Leu Lys Leu Met Gln His Thr Leu Leu Lys Ser Ala  
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Gly Gln Pro Ser Glu Pro Val Ile Thr Pro Glu Arg Ser Asp Arg Arg  
 85 90 95

Phe Lys Ala Glu Ala Trp Ser Glu Gln Pro Ile Tyr Asp Tyr Leu Lys  
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 145 150 155 160

Pro Glu Leu Leu Lys Leu Thr Leu Glu Ser Asp Gly Gln Asn Leu Val  
 165 170 175

Arg Gly Leu Ala Leu Leu Ala Glu Asp Leu Glu Arg Ser Ala Asp Gln  
 180 185 190

Leu Asn Ile Arg Leu Thr Asp Glu Ser Ala Phe Glu Leu Gly Arg Asp  
 195 200 205

Leu Ala Leu Thr Pro Gly Arg Val Val Gln Arg Thr Glu Leu Tyr Glu  
 210 215 220

Leu Ile Gln Tyr Ser Pro Thr Thr Glu Thr Val Gly Lys Thr Pro Val  
 225 230 235 240

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Pro Gln Asn Ser Leu Val Ala Trp Leu Val Ala Gln Gly Gln Thr Val  
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 340 345 350

Phe Ser Gln Pro Gly Glu Leu Gly Ile Phe Ile His Glu Pro Ile Ile  
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Ala Ala Leu Glu Ala Gln Asn Glu Ala Lys Gly Ile Met Asp Gly Arg  
 370 375 380

Gln Leu Ala Val Ser Phe Ser Leu Leu Arg Glu Asn Ser Leu Tyr Trp  
 385 390 395 400

Asn Tyr Tyr Ile Asp Ser Tyr Leu Lys Gly Gln Ser Pro Val Ala Phe  
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Asp Leu Leu His Trp Asn Ser Asp Ser Thr Asn Val Ala Gly Lys Thr  
 420 425 430

His Asn Ser Leu Leu Arg Arg Leu Tyr Leu Glu Asn Gln Leu Val Lys  
435 440 445

Gly Glu Leu Lys Ile Arg Asn Thr Arg Ile Asp Leu Gly Lys Val Lys  
450 455 460

Thr Pro Val Leu Leu Val Ser Ala Val Asp Asp His Ile Ala Leu Trp  
465 470 475 480

Gln Gly Thr Trp Gln Gly Met Lys Leu Phe Gly Gly Glu Gln Arg Phe  
485 490 495

Leu Leu Ala Glu Ser Gly His Ile Ala Gly Ile Ile Asn Pro Pro Ala  
500 505 510

Ala Asn Lys Tyr Gly Phe Trp His Asn Gly Ala Glu Ala Glu Ser Pro  
515 520 525

Glu Ser Trp Leu Ala Gly Ala Thr His Gln Gly Gly Ser Trp Trp Pro  
530 535 540

Glu Met Met Gly Phe Ile Gln Asn Arg Asp Glu Gly Ser Glu Pro Val  
545 550 555 560

Pro Ala Arg Val Pro Glu Glu Gly Leu Ala Pro Ala Pro Gly His Tyr  
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Val Lys Val Arg Leu Asn Pro Val Phe Ala Cys Pro Thr Glu Glu Asp  
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Ala Ala

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caaaaaaata aaggctgtga gtttcgagcc aataattatg aattagtggg atttttttta	180
aagataaata atcaagaatc gcattagggg gacgaatatg cgttattcaa ataaaaagac	240
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